

SCORE Search Results Details for Application 10573229 and Search Result 20090528_121103_us-10-573-229a-1.rni.

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This page gives you Search Results detail for the Application 10573229 and Search Result 20090528_121103_us-10-573-229a-1.rni.

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GenCore version 6.3
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OM nucleic - nucleic search, using sw model

Run on: May 31, 2009, 22:10:23 ; Search time 1097 Seconds
(without alignments)
5968.836 Million cell updates/sec

Title: US-10-573-229A-1
Perfect score: 920
Sequence: 1 tctgttagaggggaatggctg.....acccccaaagaaaccttcta 920

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9875436 seqs, 3558593875 residues

Total number of hits satisfying chosen parameters: 19750872

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /ABSS/Data/CRF/ptodata/1/ina/1_COMB.seq:*
2: /ABSS/Data/CRF/ptodata/1/ina/5_COMB.seq:*
3: /ABSS/Data/CRF/ptodata/1/ina/6A_COMB.seq:*
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10: /ABSS/Data/CRF/ptodata/1/ina/HB_COMB.seq:*
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13: /ABSS/Data/CRF/ptodata/1/ina/RE_COMB.seq:*
14: /ABSS/Data/CRF/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	322.2	35.0	650	9	US-09-925-065A-602935	Sequence 602935,
2	309.8	33.7	501	9	US-09-925-065A-602938	Sequence 602938,
3	149.6	16.3	485	9	US-09-925-065A-425353	Sequence 425353,
4	122.6	13.3	561	3	US-09-573-080A-108	Sequence 108, App
5	122.6	13.3	561	5	US-09-854-867-108	Sequence 108, App
6	121.2	13.2	541	3	US-09-573-080A-107	Sequence 107, App
7	121.2	13.2	541	5	US-09-854-867-107	Sequence 107, App
c 8	119.6	13.0	493	9	US-09-925-065A-176178	Sequence 176178,
c 9	119.6	13.0	504	10	US-10-301-480C-643499	Sequence 643499,
c 10	109.6	11.9	590	9	US-09-925-065A-73587	Sequence 73587, A
c 11	109.6	11.9	590	9	US-09-925-065A-73588	Sequence 73588, A
c 12	109.6	11.9	590	10	US-10-301-480C-550895	Sequence 550895,
c 13	109.6	11.9	590	10	US-10-301-480C-550896	Sequence 550896,
14	104.8	11.4	737	7	US-10-105-299-6677	Sequence 6677, Ap
15	104.8	11.4	797	7	US-10-105-299-234	Sequence 234, App
c 16	104.8	11.4	137000	3	US-10-172-911-11	Sequence 11, Appl
c 17	98.4	10.7	84105	6	US-10-741-601-5637	Sequence 5637, Ap
c 18	98	10.7	55927	3	US-09-949-016-15017	Sequence 15017, A
c 19	97.8	10.6	9245	3	US-09-949-016-13349	Sequence 13349, A
c 20	97.8	10.6	9245	3	US-09-949-016-13350	Sequence 13350, A
21	93	10.1	948	10	US-10-301-480C-92013	Sequence 92013, A
c 22	91.8	10.0	143550	3	US-09-949-016-14143	Sequence 14143, A
23	91.2	9.9	992	10	US-10-301-480C-220057	Sequence 220057,
24	90.8	9.9	76118	3	US-09-949-016-15593	Sequence 15593, A
25	90.4	9.8	806	10	US-10-301-480C-325534	Sequence 325534,
26	90.2	9.8	564	9	US-09-925-065A-236350	Sequence 236350,
27	90.2	9.8	574	10	US-10-301-480C-695058	Sequence 695058,
28	89.4	9.7	589	10	US-10-301-480C-427272	Sequence 427272,
29	89.4	9.7	589	10	US-10-301-480C-427274	Sequence 427274,
30	89.4	9.7	589	10	US-10-301-480C-605967	Sequence 605967,
31	89.4	9.7	592	9	US-09-925-065A-134131	Sequence 134131,
32	89	9.7	589	10	US-10-301-480C-427273	Sequence 427273,
33	88.4	9.6	987	10	US-10-301-480C-932619	Sequence 932619,
c 34	86.6	9.4	660	10	US-10-301-480C-296865	Sequence 296865,
c 35	85.4	9.3	870	10	US-10-301-480C-296866	Sequence 296866,
36	85.2	9.3	463	9	US-09-925-065A-594086	Sequence 594086,
37	85.2	9.3	575	9	US-09-925-065A-333372	Sequence 333372,
38	85.2	9.3	577	10	US-10-301-480C-783034	Sequence 783034,
39	85.2	9.3	986	10	US-10-301-480C-163837	Sequence 163837,
40	85.2	9.3	987	10	US-10-301-480C-950354	Sequence 950354,
41	85.2	9.3	987	10	US-10-301-480C-950355	Sequence 950355,
42	84.8	9.2	915	8	US-10-098-754-678	Sequence 678, App
43	84.2	9.2	997	10	US-10-301-480C-326425	Sequence 326425,
44	84.2	9.2	55927	3	US-09-949-016-15017	Sequence 15017, A
c 45	84	9.1	601	3	US-09-949-016-178228	Sequence 178228,

ALIGNMENTS

RESULT 1

US-09-925-065A-602935

; Sequence 602935, Application US/09925065A

; Patent No. H002191

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single

; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

; FILE REFERENCE: 108827.135

; CURRENT APPLICATION NUMBER: US/09/925,065A

; CURRENT FILING DATE: 2001-08-08

; PRIOR APPLICATION NUMBER: US 60/243,096

; PRIOR FILING DATE: 2000-10-24

; PRIOR APPLICATION NUMBER: US 60/252,147

; PRIOR FILING DATE: 2000-11-20

; PRIOR APPLICATION NUMBER: US 60/250,092

; PRIOR FILING DATE: 2000-11-30

; PRIOR APPLICATION NUMBER: US 60/261,766

; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/289,846

; PRIOR FILING DATE: 2001-05-09

; NUMBER OF SEQ ID NOS: 957086

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 602935

; LENGTH: 650

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-925-065A-602935

Query Match 35.0%; Score 322.2; DB 9; Length 650;

Best Local Similarity 95.4%; Pred. No. 1.2e-93;

Matches 354; Conservative 0; Mismatches 13; Indels 4; Gaps 2;

Qy	373	GCTGGGCGACTGAGAAGCATCACCCACTTCCCAGAACCTTTTACGTGGAGTGA	432
Db	1	GCTGGGCGACTGAGAAGCATCACCCACTTCCCAGAACCTTTTACGTGGAGTGA	60
Qy	433	TTTAAGGGGCTGTCCAGCTAAACCTCCAACCTCCAGATCCCATGCCAATTCTCTGCTTC	492
Db	61	TTTAAGGGGCTGTCCAGCTAAACCTCCAACCTCCAGATCCCATGCCAATTCTCTGCTTC	120
Qy	493	TGCAAAAGGACTTCAAGTGAAAGACATCTGCAGCTGTGAACGGGGGTAAAACCCCTCCCTG	552
Db	121	TGCAAAAGGACTTCAAGTGAAAGACATCTGCAGCTGTGAACGGGGGTAAAACCCCTCCCTG	180
Qy	553	CCCCAGGCCCAAGCAAGGATTTCCTAGCGGGGAGGAAGGTAGAATCGAGAGACCTCTA	612
Db	181	CCCCAGGCCCAAGCAAGGATTTCCTAGCGGGGAGGAAGGTAGAATCGAGAGACCTCTA	240
Qy	613	ACCTGGGAGAGGAGGGAGGAAATCTCCGAGGACCAGGGTTATGCAACAACACAAGGGA	672
Db	241	ACCTGGGAGAGGAGGGAGGAAATCTCCGAGGACCAGGGTTATGCAACAACACAAGGGA	300
Qy	673	AGTACCTGTGGGTTTGGGGTTGGGGAAGGAAATCCCTACTGCCCAAGAGCCAGCC	732

Db 301 AGTACCTGTCTGG---TTCTGGGGTTGGGGAGGAAGATCCCTACTG-CCCAAGAGCCAGCA 356

Qy 733 CCGAACCCAAG 743
| | | | |

Db 357 CAGACACAAGG 367

RESULT 2

US-09-925-065A-602938

; Sequence 602938, Application US/09925065A

; Patent No. H002191

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single

; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

; FILE REFERENCE: 108827.135

; CURRENT APPLICATION NUMBER: US/09/925,065A

; CURRENT FILING DATE: 2001-08-08

; PRIOR APPLICATION NUMBER: US 60/243,096

; PRIOR FILING DATE: 2000-10-24

; PRIOR APPLICATION NUMBER: US 60/252,147

; PRIOR FILING DATE: 2000-11-20

; PRIOR APPLICATION NUMBER: US 60/250,092

; PRIOR FILING DATE: 2000-11-30

; PRIOR APPLICATION NUMBER: US 60/261,766

; PRIOR FILING DATE: 2001-01-16

; PRIOR APPLICATION NUMBER: US 60/289,846

; PRIOR FILING DATE: 2001-05-09

; NUMBER OF SEQ ID NOS: 957086

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 602938

; LENGTH: 501

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-925-065A-602938

Query Match 33.7%; Score 309.8; DB 9; Length 501;

Best Local Similarity 94.5%; Pred. No. 1.1e-89;

Matches 343; Conservative 0; Mismatches 17; Indels 3; Gaps 2;

Qy 381 ACTGAGAAGCATCACCCACTTCCCCAGAACCTTTTTTACGTGGAGTGAAGAACTTTAAGGG 440
| | | | |

Db 1 ACTGAGAAGCATCACCCACTTCCCCAGAGCCTTTTTTACATGGAGTGAAGAACTTTAAGGG 60

Qy 441 GCTGTCCAGCTAAACCTCCAACCTCCAGATCCCATGCCAATTTCTCTGCTTCTGCAAAAG 500
| | | | |

Db 61 GCTGTCCAGCTAAACCTCCAACCTCCAGATCCCATGCCAAGTTCTCTGCTTCTGCAAAAG 120

Qy 501 GACTTCAAGTGAAGAGACATCTGCAGCTGTGAACGGGGGTAAAACCTCCCTGCCCCAGGC 560
| | | | |

Db 121 GACTTCAAGTGAAGAGACATCTGCAGCTGTGAACGGGGGTAAAACCTCCCTGCCCCAGGC 180

Qy 561 CCCAAGCAAGGATTTCCTAGCGGGGAGGAAGGTAGAATCGAGAGACCTCTAACCCCTGGG 620
| | | | |

Db 181 CCCAAGCAAGGATTTCCTAGCGGGGAGGAAGGTAGAATCGAAAGACCTCTAACCCCTGGG 240

Qy 621 AGAGGAGGGAGGGAAATCTCCGAGGACAGGGTTATGCAACAACACAAGGAAGTACCTG 680

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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      241  AGAGGAGGGAGGGAAATCTCCGAGGACAGGGTTATGCAACAACACAGGGGAAGTACCTG 300

Qy      681  CTGGGTCTCGGGGTGGGGGAAGGAAATCCCTACTGCCCCAAGAGCCAGCCCCGAACCC 740
                |||||  |  |||||  ||  |||||  |||||||||||  |||||||||||  ||  |
Db      301  CTGG--TTCTGGGGTCAGGGAGGAAGATCCCTACTG--CCCAAGAGCCAGCACAGACACA 357

Qy      741  AAG 743
                |  |
Db      358  AGG 360

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RESULT 3

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US-09-925-065A-425353
; Sequence 425353, Application US/09925065A
; Patent No. H002191
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 425353
; LENGTH: 485
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-425353

```

```

Query Match          16.3%; Score 149.6; DB 9; Length 485;
Best Local Similarity 91.0%; Pred. No. 1.5e-37;
Matches 193; Conservative 0; Mismatches 14; Indels 5; Gaps 3;

```

```

Qy      532  ACGGGGGTAAACCTCCCTGCCCCAGGCCCCAAGCAAGGATTTCCCTAGCGGGGAGGAA 591
                |||||||||||  |||||||||||  |||||||||||  |||||||||||  |||||||||||
Db      1    ACGGGGGTAAACCTTCCCTGCCCCAGGCCCCAAGCAAGGATTTCCCTAGCGGGGAGGAA 60

Qy      592  GGTAGAATCGAGAGACCTCTAACCTGGGAGAGGAGGGAGGAAATCTCCGAGGACCAGG 651
                |||||||||||  |||||||||||  |||||||||||  |||||||||||  |||||||||||
Db      61  GGTAGAATCGAGAGACCTCTAA--CCTGGGAGAGGAGGGAGGAAATCTCCGAGGACCAGG 119

Qy      652  GTTATGCAACAACACAGGGAAGTACCTGCTGGGTCTGGGGTTGGGGAAGGAAATCC 711
                |||||||||||  |||||||||||  |||||||||||  ||  ||  ||  ||  ||  ||  ||
Db      120  GTTATGCAACAACACAGGGAAGTACCTGCTGG---TTCTGGGGTTGGGAGGAAGATCC 176

```



```

Db          321 ACAGCCATGTGAGTGAGCCATCTTGAAGCAGATCCTCCAGCCCCAGTCAAGCCTTCAGA 380
Qy          168 TGGCTGCAGCCACAGCCAAACAAGACTGCAACCTCCTGGGGGATCCTGAGCCAGAATC 227
            || ||||| |||| |||| | ||||| || | || ||||| |||| |
Db          381 TGACTGCAGCCCCAGCTAACATCTTGACTGCAACCTCATGAGAGACCTGAGCCAGAACC 440
Qy          228 CCCTGGCTAAATTGCTCCTTGATTCTTAACCCACAGAAATTGTGTAAGA 276
            || |||| | |||| | |||| | ||||| |||| |||
Db          441 ACCCAGCTAAGCTGCTCCTAAATTCCTGACCCACAGAACTGTGAGAGA 489
    
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RESULT 5

```

US-09-854-867-108
; Sequence 108, Application US/09854867
; Patent No. 7014997
; GENERAL INFORMATION:
; APPLICANT: JOAN, KNOLL H
; APPLICANT: ROGAN, PETER K
; TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING
SAME
; FILE REFERENCE: 30307
; CURRENT APPLICATION NUMBER: US/09/854,867
; CURRENT FILING DATE: 2003-05-08
; NUMBER OF SEQ ID NOS: 613
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 108
; LENGTH: 561
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: (1)..(561)
; OTHER INFORMATION: mlt1f1
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (62)..(62)
; OTHER INFORMATION: n is a, c, g or t
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (165)..(165)
; OTHER INFORMATION: n is a, c, g or t
US-09-854-867-108
    
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Query Match          13.3%; Score 122.6; DB 5; Length 561;
Best Local Similarity 69.6%; Pred. No. 1e-28;
Matches 201; Conservative 0; Mismatches 74; Indels 14; Gaps 2;
    
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```

Qy          2 CTGTAGAGGGGAATGGCTGCTGTGTCATGGGGGTGCATGAGCAGCCCACTGGAGAGGTGC 61
            || | | | | |||| | |||| | | | ||||| ||||| |
Db          201 CTCTGGGGGAAGCCAGCTGCCATGTGTCATGAGGACACTCAAGCAGCCCTGTGGAGAGGCCCC 260
Qy          62 ACTTGGTGAGAAACCGATGCCT-CTGCCAACCACTGCACTAACCTGCTGGGTC----- 114
            | ||| || ||| || |||| | |||| | ||| | ||
Db          261 ATGTGGCAAGGAAGTCTGAGCCTCCTGCCAACAGCCAGCAAGGAAGTCTGAGCCTCTCTGCCA 320
Qy          115 -----TGAGACTGAGCCACTTTGGAAGCTGATCTTGAGGACCACTGAGCCCTTAGC 167
            || | ||||| | |||| | ||| | | ||||| || | ||
    
```

```

Db          321 ACAGCCATGTGAGTGAGCCATCTTGAAGCAGATCCTCCAGCCCCAGTCAAGCCTTCAGA 380
Qy          168 TGGCTGCAGCCACAGCCAAACAAGACTGCAACCTCCTGGGGGATCCTGAGCCAGAATC 227
            || ||||| |||| |||| | ||||| |||| | || ||||| |||| |
Db          381 TGACTGCAGCCCCAGCTAACATCTTGACTGCAACCTCATGAGAGACCTGAGCCAGAACC 440
Qy          228 CCCTGGCTAAATTGCTCCTTGATTCTTAACCCACAGAAATTGTGTAAGA 276
            || |||| | |||| | |||| | ||||| |||| | |||
Db          441 ACCCAGCTAAGCTGCTCCTAAATTCCTGACCCACAGAACTGTGAGAGA 489
    
```

RESULT 6

US-09-573-080A-107

; Sequence 107, Application US/09573080A

; Patent No. 6828097

; GENERAL INFORMATION:

; APPLICANT: JOAN, KNOLL

; APPLICANT: ROGAN, PETER

; TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING SAME

; FILE REFERENCE: 30307

; CURRENT APPLICATION NUMBER: US/09/573,080A

; CURRENT FILING DATE: 2000-05-16

; NUMBER OF SEQ ID NOS: 479

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 107

; LENGTH: 541

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: repeat_region

; LOCATION: (1)..(541)

; OTHER INFORMATION: mltlf

; NAME/KEY: misc_feature

; OTHER INFORMATION: n is a, c, g or t

; PUBLICATION INFORMATION:

; PUBLICATION INFORMATION:

; AUTHORS: Jurka, J; Walichiewicz, J; Milosavljevic, A

; TITLE: Prototypic sequences for human repetitive DNA

; JOURNAL: Journal of Molecular Evolution

; VOLUME: 35

; ISSUE: 4

; PAGES: 286-291

; DATE: 1992-10-__

; DATABASE ACCESSION NUMBER: Database of repetitive elements (repbase)

; DATABASE ENTRY DATE: ____-__-__

; DATABASE ENTRY DATE: 1996-01-26

US-09-573-080A-107

Query Match 13.2%; Score 121.2; DB 3; Length 541;

Best Local Similarity 68.8%; Pred. No. 2.8e-28;

Matches 190; Conservative 3; Mismatches 81; Indels 2; Gaps 2;

```

Qy          2 CTGTAGAGGGGAATGGCTGCTGTGTCATGGGGTGCATGAGCAGCCCCAGTGGAGAGGTGC 61
            || |||| | |||| | ||| | | ||||| | ||||| |||
Db          197 CTCTGGGGGAAGCCAGCTGCCATGCTATGAAGACACTCAAGCAGCCTA-TGGAGAAGTCC 255
    
```



```

Qy          62 ACTTGGTGAGAAACCGATGCCT-CTGCCAACACCTGCACTAACCTGCTGGGTCTGAGAC 120
           || ||| || ||| || | || ||||| || || ||: ||| | || ||
Db          256 ACGTGGSAAGGAAGTCTGAGGTCTCTGCCAACAGCCAGCTTCGACYTGCCAGCCATGTGAG 315

Qy          121 TGAGCCACTTTGGAAGCTGATCTTGAGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCAC 180
           || ||| || ||||| ||||| || || ||||| ||||| || ||||| ||
Db          316 TGAGCCATCTTGAAGCGGATCCTCCAGCCCCAGTYAAGCCTTCAGATGACTGCAGCCCC 375

Qy          181 AGCCAACAACAAGACTGCAACCTCTGGGGGATCCTGAGCCAGAATCCCTGGCTAAATT 240
           || ||| | ||||| ||||| || | || ||||| ||||| || ||||| |
Db          376 GGCTGACATCTTGACTGCAACCTCATGAGAGACCTGAGCCAGAATAACCCAGCTAAGCT 435

Qy          241 GCTCCTTGATTCTTAACCCACAGAAATTGTGTAAGA 276
           ||||| :||| | ||||| ||||| |||| | |
Db          436 GCTCCTARATTCTGACCCACAGAACTGTGAGATA 471

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RESULT 7

US-09-854-867-107

; Sequence 107, Application US/09854867

; Patent No. 7014997

; GENERAL INFORMATION:

; APPLICANT: JOAN, KNOLL H

; APPLICANT: ROGAN, PETER K

; TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATING SAME

; FILE REFERENCE: 30307

; CURRENT APPLICATION NUMBER: US/09/854,867

; CURRENT FILING DATE: 2003-05-08

; NUMBER OF SEQ ID NOS: 613

; SOFTWARE: PatentIn version 3.1

; SEQ ID NO 107

; LENGTH: 541

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: repeat_region

; LOCATION: (1)..(541)

; OTHER INFORMATION: mltif

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (179)..(179)

; OTHER INFORMATION: n is a, c, g or t

US-09-854-867-107

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Query Match          13.2%; Score 121.2; DB 5; Length 541;
Best Local Similarity 68.8%; Pred. No. 2.8e-28;
Matches 190; Conservative 3; Mismatches 81; Indels 2; Gaps 2;

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```

Qy          2 CTGTAGAGGGGAATGGCTGCTGTGTCATGGGGGTGCATGAGCAGCCAGTGGAGAGGTGC 61
           || ||| || ||||| || ||| || || ||||| ||||| ||||| ||
Db          197 CTCTGGGGGAAGCCAGCTGCCATGCTATGAAGACACTCAAGCAGCCTA-TGGAGAAGTCC 255

Qy          62 ACTTGGTGAGAAACCGATGCCT-CTGCCAACACCTGCACTAACCTGCTGGGTCTGAGAC 120
           || ||| || ||| || | || ||||| || || ||: ||| | || ||
Db          256 ACGTGGSAAGGAAGTCTGAGGTCTCTGCCAACAGCCAGCTTCGACYTGCCAGCCATGTGAG 315

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http://es.ScoreAccessWeb/GetItem.action?AppId=105732...8_121103_us-10-573-229a-1.rni&ItemType=4&startByte=0 (10 of 17)6/15/2009 10:36:32 AM

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Qy      181  AGCCAACAACAAGACTGCAACCTCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATT 240
        ||| ||| | | ||||| | | ||| ||||| | | ||| :|||
Db      239  AGCTGACATCTTGGCTGCAACCCACGAGGGAATCTGAGCCAGCACCACCAAGMTAAGCC 180

Qy      241  GCTCCTTGATTCCTTAACCCACAGAAATTGTGTAAGA 276
        ||||| |||| | || ||||| |||| | |
Db      179  ACTCCTAAATTCCTGACTTGCAGAAAATGTGTGAAA 144

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RESULT 9

US-10-301-480C-643499/c

; Sequence 643499, Application US/10301480C

; Patent No. H002220

; GENERAL INFORMATION:

; APPLICANT: Wang, David G.

; TITLE OF INVENTION: Identification and Mapping of Single

; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome

; FILE REFERENCE: 108827-137

; CURRENT APPLICATION NUMBER: US/10/301,480C

; CURRENT FILING DATE: 2002-11-21

; PRIOR APPLICATION NUMBER: US 10/215,598

; PRIOR FILING DATE: 2002-08-09

; PRIOR APPLICATION NUMBER: US 60/311,695

; PRIOR FILING DATE: 2001-08-10

; NUMBER OF SEQ ID NOS: 989478

; SOFTWARE: FastSEQ for Windows Version 4.0

; SEQ ID NO 643499

; LENGTH: 504

; TYPE: DNA

; ORGANISM: Homo sapiens

US-10-301-480C-643499

Query Match 13.0%; Score 119.6; DB 10; Length 504;
 Best Local Similarity 66.7%; Pred. No. 9.1e-28;
 Matches 184; Conservative 1; Mismatches 90; Indels 1; Gaps 1;

```

Qy      2   CTGTAGAGGGGAATGGCTGCTGTGTGCATGGGGGTGCATGAGCAGCCCAAGTGGAGAGGTTGC 61
        || | |||| | ||||| ||||| ||| | | ||||| ||||| ||| | ||||| ||||| ||| | |||||
Db      430  CTCTGGAGGAAGTCAGCTGCTGTGTGCATGAGGGCACTCAAACAGCCCTATGAAGAGGTCC 371

Qy      62  ACTTGGTGAGAAACCGATGCC-TCTGCCAACCACTGCACTAACCTGCTGGGTCTGAGAC 120
        | |||| | ||| || | | ||||| || ||| |||| | ||| |||| | ||| |||| |
Db      370  ATGTGGTAAGGAACTGAGGACTTCTGCCAACAGCCAGCAATAAAGTGGCCAGGTATGTGAA 311

Qy      121  TGAGCCACTTTGGAAGTGATCTTGGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCAC 180
        || |||| | ||||| | | | | |||| | || | ||| |||| |
Db      310  TGTGCCATCTTGAAGCAAGTTCTCCAAGTCCAGACAAGCTCTCTAATAAGTGTGGCCCC 251

Qy      181  AGCCAACAACAAGACTGCAACCTCCTGGGGGATCCTGAGCCAGAATCCCCTGGCTAAATT 240
        ||| ||| | | ||||| | | ||| ||||| | | ||| ||||| | | ||| :|||
Db      250  AGCTGACATCTTGGCTGCAACCCACGAGGGAATCTGAGCCAGCACCACCAAGMTAAGCC 191

Qy      241  GCTCCTTGATTCCTTAACCCACAGAAATTGTGTAAGA 276
        ||||| |||| | || ||||| |||| | |
Db      190  ACTCCTAAATTCCTGACTTGCAGAAAATGTGTGAAA 155

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; Sequence 73588, Application US/09925065A
; Patent No. H002191
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827.135
; CURRENT APPLICATION NUMBER: US/09/925,065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243,096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252,147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250,092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261,766
; PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 73588
; LENGTH: 590
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-73588

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Query Match          11.9%; Score 109.6; DB 9; Length 590;
Best Local Similarity 63.8%; Pred. No. 1.8e-24;
Matches 166; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

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Qy      17 GCTGCTGTGCATGGGGGTGCATGAGCAGCCAGTGGAGGGTGCACCTTGGTGAGAAACC 76
      ||| || ||||| || || |||| | |||| | ||| |||
Db      299 GCTTCCATGTGCATGAGGATATTCCAGCAATTCTATTAAAGAGTCCACATGGCAAGGAACCTG 240

Qy      77 GATGCTCTGCCACACCACTGCACTAACCTGCTGGGTCTGAGACTGAGCCACTTTGGAAG 136
      | ||||| ||| ||| |||| | ||| ||| ||| ||||| |||
Db      239 AGGTCCTTCTGCCACACCAAGCATTAAACATTCCAGGCTTGTGGGTGAGTCCCTTTGGAAG 180

Qy      137 CTGATCTTGGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCACAGCCAACAACAAGACT 196
      | |||| | || ||||| ||| || || ||||| ||| | ||| ||
Db      179 CAGATCCTCCAGACTCAGTCAAGCCATCAGATGACTGCAGTCCAGGTGATGCCCAAGCT 120

Qy      197 GCAACCTCCTGGGGGATCCTGAGCCAGAATCCCTGGCTAAATTGCTCCTTGATTCTTAA 256
      ||||| ||| ||||| ||||| ||| ||| ||| ||| ||| |||
Db      119 GCAACCTCAAGAAAGATCCTGAGCCAGAACCAGTCAAGTAGCTCTCAGGTTCTCTGA 60

Qy      257 CCCACAGAAATTGTGTAAGA 276
      || |||| || |||| |||
Db      59 CCTACAGCAACTGTGTGAGA 40

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RESULT 12
US-10-301-480C-550895/c
; Sequence 550895, Application US/10301480C
; Patent No. H002220
; GENERAL INFORMATION:

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; PRIOR FILING DATE: 2001-08-10
; NUMBER OF SEQ ID NOS: 989478
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 550896
; LENGTH: 590
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-301-480C-550896

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Query Match          11.9%; Score 109.6; DB 10; Length 590;
Best Local Similarity 63.8%; Pred. No. 1.8e-24;
Matches 166; Conservative 0; Mismatches 94; Indels 0; Gaps 0;

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Qy      17 GCTGCTGTGCATGGGGGTGCATGAGCAGCCAGTGGAGGGTGCACTTGGTGAGAAACC 76
         ||| | ||||| || | ||| | ||| | ||| | ||| |
Db      299 GCTTCCATGTGCATGAGGATATTCCAGCAATTCTATTAAAGAGTCCACATGGCAAGGAACTG 240

Qy      77 GATGCTCTGCCAACCACTGCCTGCTGGGTCTGAGACTGAGCCACTTTGGAAG 136
         | ||||| ||| ||| ||| | || | ||| | ||| | ||| |
Db      239 AGGTCCTTCTGCCAACCAACAGCATTAAACATTCCAGGCTTGTGGGTGAGTCCCTTTGGAAG 180

Qy      137 CTGATCTTGGAGCACCAGTCAAGCCCTTAGCTGGCTGCAGCCACAGCCAACAACAAGACT 196
         | ||| | || | ||||| ||| | || | ||| | ||| | ||| |
Db      179 CAGATCCTCCAGACTCAGTCAAGCCATCAGATGACTGCAGTCCCAAGTGATGCCCAAGCT 120

Qy      197 GCAACCTCCTGGGGGATCCTGAGCCAGAATCCCTGGCTAAATTGCTCCTTGATTCTTAA 256
         ||||| | | ||||| ||| | ||| | ||| | ||| | ||| |
Db      119 GCAACCTCAAGAAAGATCCTGAGCCAGAACCAGTCAAGTCTCAGGTTCTCTGA 60

Qy      257 CCCACAGAAATTGTGTAAGA 276
         || ||| || ||||| |||
Db      59 CCTACAGCAACTGTGTGAGA 40

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RESULT 14

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US-10-105-299-6677
; Sequence 6677, Application US/10105299
; Patent No. 7368527
; GENERAL INFORMATION:
; APPLICANT: Rosen, et. al
; TITLE OF INVENTION: Human Secreted Proteins
; FILE REFERENCE: PS950
; CURRENT APPLICATION NUMBER: US/10/105,299
; CURRENT FILING DATE: 2002-03-26
; NUMBER OF SEQ ID NOS: 15197
; Prior Application removed - See File Wrapper or Palm
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6677
; LENGTH: 737
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-105-299-6677

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Query Match          11.4%; Score 104.8; DB 7; Length 737;
Best Local Similarity 68.5%; Pred. No. 7.3e-23;
Matches 174; Conservative 0; Mismatches 77; Indels 3; Gaps 2;

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      | | | | | | | | | | | | | | | | | | | | | | | |
Db      563 TCATGAGAGA--CTGAGCCACAACAACCTAGCTAAGAAGTCCTGAATTCCTACCAACA 620

Qy      263 GAAATTGTGTAAGA 276
      | | | | | | | | | | | | | | | | | | | | | | | |
Db      621 GAAACTATGTGAGA 634
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Search completed: May 31, 2009, 22:28:46

Job time : 1103 secs

SCORE 34